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The Social Determinants of Health and Space-Time Clustering of COVID-19 Cases in the United States Veteran Population

By

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An abstract of
A thesis submitted to the Faculty of the
Rollins School of Public Health of Emory University
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Abstract

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Introduction: Disparities in COVID-19 outcomes are demonstrated globally and in the United States (U.S.). However, less is known about the spatial distribution and clustering of cases in the U.S. The U.S. Department of Veteran's Affairs (VA) offers a comprehensive dataset with COVID-19 incidence that allows for county-level spatial analysis in conjunction with social determinants of health.

Methods: Data for 6,342,455 Veterans who utilized VA services between January 1, 2018 and September 30, 2021 were assessed for COVID-19 testing and test positivity. Analysis examined characteristics of all Veterans who received care, and by those who received at least one COVID-19 test or at least one positive COVID-19 test. Maps were produced that indicated testing and positivity rates by county. Using SaTScan software, a spatial cluster analysis was conducted over space and time to identify where and when Veterans were most at risk of COVID-19 test positivity.

Results: Of the 6,342,455 Veterans who utilized VA services during the study period, 1,352,736 (21.33%) received at least one COVID-19 test, and 275,863 (20.4%) of those tested received at least one positive COVID-19 test. Non-Hispanic Black and Hispanic Veterans were more likely to receive at least one COVID-19 test than their white counterparts, and Hispanic Veterans were more likely to receive at least one positive COVID-19 test than their non-Hispanic counterparts. County-level maps suggested that testing rates may cluster around VA facilities. Space-time cluster analysis indicated that Veterans were most at risk of testing positive between November 2020 and January 2021 in the Midwest, compared to those who received testing outside of the identified cluster (RR: 3.45, $p < .001$).

Discussion: Results indicate areas and time periods in the continental U.S. where Veterans were at increased risk of testing positive. Findings align with existing literature on clusters of COVID-19 cases in the general U.S. population but additional analysis is needed to understand patterns during the Delta and Omicron variant-predominant periods. These findings and methods can be extended as the pandemic progresses and in smaller geographic areas to inform VA policy and resource allocation.

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I. Background

As of April 12, 2022, there have been over 497 million confirmed cases of COVID-19 worldwide and over 6.1 million deaths due to COVID-19 reported to the World Health Organization (WHO) (World Health Organization, n.d.-b). Throughout the pandemic, research has examined the role of social determinants of health (SDOH) on COVID-19 test positivity, hospitalization, and mortality. The World Health Organization defines the social determinants of health as ‘non-medical factors’ that impact health outcomes (World Health Organization, n.d.-a). SDOH that are typically examined in the context of COVID-19 are education, income, race, ethnicity, gender, marital status and neighborhood deprivation or a measure of urbanicity. COVID-19 test positivity has been found to be associated with income, race, gender and urban residence, but this list is not conclusive and there is wide variation in study designs and study populations (Ferguson, Abdel Magid, Purnell, Kiang, & Osborne, 2021; Rentsch, Kidwai-khan, et al., 2020).

In the United States there have been over 80 million COVID-19 cases and over 982,000 deaths due to COVID-19 as of April 12, 2022 (Centers for Disease Control and Prevention, n.d.). Several studies in the literature have examined social determinants of health and COVID-19 outcomes in the United States. In one cross-sectional study using data from 20,899 patients in the Mount Sinai Health System, positive test results were significantly associated with patients who were older, male, racial/ ethnic minorities, current smokers, non-primary English speakers, or those who had comorbidities. Of note, study participants of African ancestry were at statistically significant higher risk of each of the four outcomes of test positivity, hospitalization, intubation and mortality (Lundon et al., 2020).

There have been several retrospective cohort studies using data from health surveillance systems in the United States. One study examined data from 92 hospitals in 12 states across the United States and found that hospitalized Black patients had more comorbid conditions than hospitalized white patients. Racial differences were largely explained by patient sociodemographic and comorbid conditions and medical insurance status was the strongest predictor of mortality (Yehia et al., 2020). Another study including 12,866 individuals from the University of Michigan health system, found that Black patients were more likely to obtain testing, have a positive test result, and be hospitalized than white patients. Additionally, patients who lived in areas with higher population density had an increased risk of hospitalization compared to those living in lower population density areas (Gu et al., 2020). In northern California, data from 1,052 confirmed COVID-19 cases in the Sutter Health system indicated that Black patients had nearly double the odds of hospitalization than their white counterparts (Azar et al., 2020). Finally, another study examining data for 3,626 COVID-19- positive patients in the Ochsner Health system in Louisiana, found that Black patients had nearly a two-fold increase in odds of hospital admission when compared to white patients (Price-Haywood, Burton, Fort, & Seoane, 2020).

There are limitations to studies that utilize single health system data. First, they are limited in their use of singular surveillance or health system records. As a result, study sample sizes are relatively small and subject to limitations in generalizability. Second, studies have been conducted in local or regional geographic areas, and do not span across the United States. Therefore, further research is needed to understand the relationship between SDOH and COVID-19 outcomes in larger populations and geographic areas across the United States.

The United States Department of Veterans Affairs (VA) has large administrative datasets representing Veterans' health care utilization data from hospitals, clinics and community health centers across the United States. Further, the VA collects extensive social determinants of health and comorbidity variables over time at the individual level, such as income, number of people in the household, education and many others. To date, several studies have been conducted examining SDOH and COVID-19 outcomes in the United States Veteran population. These studies have focused on different outcomes including COVID-19 test access and positivity, hospitalization, and mortality.

Research in the VA population has consistently demonstrated that Black Veterans are more likely than white Veterans to be tested and to test positive for COVID-19. Of note, four national retrospective cohort studies have been conducted using VA data to assess COVID-19 testing access and positivity (Ferguson et al., 2021; Ioannou et al., 2020; Razjouyan et al., 2021; Rentsch, Kidwai-Khan, et al., 2020). One study analyzed data for 6,292,800 veterans, and found that Black Veterans comprised 17.5% of the cohort but made up 23.2% of those tested and 25.8% of those who tested positive for COVID-19. Further, all non-white racial categories were at increased risk of receiving a positive COVID-19 test result when compared to non-white Veterans (Ferguson et al., 2021). Another study analyzed data for 2,026,227 Veterans and found that Black Veterans were twice as likely to get tested when compared to white Veterans and 2.5 times as likely to test positive for COVID-19 than non-Black Veterans (Rentsch, Kidwai-khan, et al., 2020). Using data for 5,834,543 Veterans, another research team found that Black/ Hispanic individuals were more likely to be tested and to test positive for COVID-19 than their white counterparts, after adjusting for a wide range of social determinants of health and medical comorbidity variables (Rentsch, Kidwai-Khan, et al., 2020). Lastly, another study of 88,747 patients tested at the VA found that those who tested positive were older, more likely to be Black, more likely to be obese, and more likely to live in a State with higher COVID-19 burden (Ioannou et al., 2020).

Other retrospective cohort studies have examined hospitalization and mortality in the VA population. In a dataset of 8,667,996 active Veterans, among the 252,702 who were tested, Black and Hispanic patients were 1.9 times and 1.4 times as likely to be hospitalized than white patients, respectively, after adjusting for age, sex, and comorbidities using the Elixhauser comorbidity index (Razjouyan et al., 2021). In another study of 88,747 VA patients, among those who tested positive, older age, higher regional COVID-19 disease burden, higher Charlson comorbidity index, and other medical conditions upon admission were found to be significantly associated with mortality (Ioannou et al., 2020).

While existing studies in the literature describe associations between SDOH and COVID-19 outcomes, the majority of studies primarily look at race and COVID-19 outcomes. It is important to consider that SDOH such as race are not inherently exposure variables. Rather, variables such as race can serve as proxies for experiences of racism and structural inequality (Maness et al., 2021). Including other social determinants of health in analyses is a critical step to better understand how race can or cannot be causally linked to COVID-19 outcomes. Further, analyzing SDOH and COVID-19 cases at the county-level is one tool that can be used to assess the role of an individual's environment on their health outcomes.

There is evidence that county-level SDOH are associated with geographic variation in COVID-19 incidence. Specifically, two cross-sectional studies found geographic variation in COVID-19 cases across the United States and that counties with higher proportions of people of color had higher rates of COVID-19 diagnoses (Millett et al., 2020; Rodriguez-Diaz et al., 2020).

One of these studies stratified United States counties by percentage of Black residents and found that counties with more than 5% Black residents had higher rates of COVID-19 diagnoses, compared with counties with less than 5% Black residents after adjusting for age, poverty, comorbidities and epidemic duration at the county-level (Millett et al., 2020). In the other study using similar methods, findings indicated that particularly in Northeast and Midwest regions, counties with higher proportions of Latino residents had higher rates of COVID-19 cases, after adjusting for age, percent unemployed, percent uninsured and other SDOH characteristics, as well as medical comorbidities (Rodriguez-Diaz et al., 2020).

There is also evidence suggesting that county-level SDOH factors are associated with geographic variability in COVID-19 cases and deaths. In analyzing 2,814 United States counties, findings indicated that large metropolitan areas have experienced the most cases and deaths, but that there has been a disproportionate impact on some smaller cities across the United States. Regression analysis results found that population density, percentage of residents over the age of 65, and percentage of the population that was tested were statistically significantly correlated with COVID-19 cases (Zhang & Schwartz, 2020). In another study, researchers used county-level COVID-19 mortality data and found that residential segregation, higher percentages of Black residents, and female residents were associated with higher rates of COVID-19 mortality (Paul, Arif, Pokhrel, & Ghosh, 2021). Lastly, one study used county-level data and found that income inequality had a weak positive correlation with increased numbers of cases and deaths per 100,000 people (Tan, Hinman, Abdel Magid, Nelson, & Odden, 2021). Assessment of SDOH at the county-level is an important tool to address the ways in which context and environment can be associated with COVID-19 community-level incidence.

However, in using county-level variables, associations between SDOH and COVID-19 incidence may not be representative of individual level risk factors. By assessing how one geographic region's COVID-19 burden is related to nearby geographic region's COVID-19 burden, researchers can partially account for existing limitations of little to no availability of individual level SDOH (Andrews et al., 2021; Kim & Bostwick, 2020; Maroko, Nash, & Pavilonis, 2020; Saffary et al., 2020). In one cluster analysis at the county-level in the United States, findings indicated that there was significant global spatial correlation between the percentage of Black residents and COVID-19 cases and deaths and that there was a significant but weak spatial correlation between the number of ICU beds and COVID-19 cases and deaths (Saffary et al., 2020). Another cluster analysis used ZIP Code Tabulation Areas in New York City and Chicago and found that 'cold' spots (low incidence areas) were wealthier, had a higher proportion of non-Hispanic white residents and had a higher prevalence of SDOH of health that are commonly associated with positive health outcomes. Hot spots (areas of high incidence) were found to have higher proportions of people of color and people with less than a college degree (Maroko et al., 2020).

Few studies have examined spatial dependence over time. One study conducted a cluster analysis using county-level data at four different time points, with the last one ending on April 30, 2021. Findings indicated that spatial variation in COVID-19 outcomes varied over time and that rural counties were increasingly included in clusters as the pandemic progressed. Further, while counties with higher percentages of whites were not included in clusters until the third period, counties with higher percentages of people of color were consistently included in clusters throughout all four periods (Andrews et al., 2021). Another study analyzed clusters of COVID-19 cases at the county-level over space and time, and found that a county being in a cluster was associated with urbanicity, short distance to airports, population size, and proportion of racial/ ethnic minorities (Wang, 2020).

Regression models that include spatial variables have also been used to understand the role of space in the proliferation of the COVID-19 pandemic. After analyzing 35 potential explanatory variables and COVID-19 incidence at the county-level in the United States, four explanatory variables were identified to be the best predictors of COVID-19 incidence: income inequality, median household income, percentage of nurse practitioners and percentage of Black female residents. After incorporating spatial dependence into models, the ability for the models to predict COVID-19 incidence improved. Further, income inequality was particularly influential in predicting COVID-19 incidence in the tri-state area and both local models were poor at predicting COVID-19 incidence in States in the Southwest and in most of the Northern Great Plains (Mollalo, Vahedi, & Rivera, 2020).

In summary, there is considerable evidence in the literature that SDOH are associated with COVID-19 outcomes and that there is geographic variation and spatial heterogeneity in COVID-19 outcomes in United States counties. Notably, there is limited literature on the spatial distribution and clustering of COVID-19 incidence in the U.S. Veterans population. Understanding how and where U.S. Veterans were most affected by COVID-19 can inform future policy and have implications for VA service delivery. Overall, the goal of this analysis is to further understand the distribution of COVID-19 cases in the U.S. Veterans population. First, we aim to describe the SDOH and demographics of the U.S. Veterans population in our study period. Second, we aim to identify clusters in space and time of COVID-19 cases in the U.S. Veterans population in order to understand where and how the COVID-19 pandemic affected U.S. Veterans.

II. Methods

A. Study Design

The United States Department of Veterans Affairs (VA) is the largest integrated healthcare system in the United States and serves 9 million Veterans each year in 1,293 healthcare facilities throughout the United States (U.S. Department of Veterans Affairs, n.d.). We conducted a cross-sectional analysis of Veterans who received care at the VA prior to the beginning of or during the COVID-19 pandemic and who received COVID-19 testing at the VA. This study was approved by the VA Institutional Review Board and was granted a waiver of informed consent.

B. Study Population

Eligible study participants were Veterans who had at least one hospital inpatient stay or outpatient encounter between January 1, 2018, and September 30, 2021. In order to collect information about the baseline Veteran population, Veterans who utilized services before the beginning of the COVID-19 pandemic were included. Information regarding COVID-19 testing was retrieved on December 1, 2021, and all individuals who had received a COVID-19 test were included in the final analytic dataset.

C. Data Sources

Four data sources were used for this analysis: 1) The VA Corporate Data Warehouse (CDW) which is a centralized network of health information for Veterans in the United States; 2) The United States Veterans Eligibility Trends and Statistics (USVETS) database which contains over 250 individual-level variables from over 35 data sources and was utilized for social determinants of health variables in this analysis. USVETS is a relatively new dataset, and few researchers have used this data source to date; 3) COVID-19 Shared Data Resource (CSDR) which is a centralized collection of data that was implemented by the VA in April of 2020 to systematically capture COVID-19-related data across the VA data infrastructure; and 4) The U.S. Census American Community Survey (ACS) 5-year estimates for 2014 through 2019 were utilized for county-level geographic data (United States Census Bureau, n.d.).

D. Data Measures

Outcome Variable

The primary outcome of interest for this analysis was COVID-19 test positivity, retrieved from the CSDR. We utilized a binary variable indicating whether each Veteran received a COVID-19 test and the result of the first COVID-19 test on record. If a Veteran did not receive any testing, the variable was coded as missing. The variable was coded as "1" if the Veteran received at least one positive test and as "0" if the Veteran received no positive tests. The index date for each Veteran was identified as the date of the first positive test or the date of the first negative test, if no positive test was recorded. In the case that a Veteran received multiple tests, the index date only recorded the date of the first test.

Demographic Variables

Demographic variables were retrieved from the CDW and CSDR, including race, ethnicity, age, and gender. Race and ethnicity were combined and categories included: Non-Hispanic white, Non-Hispanic Black or African American, Asian, American-Indian or Alaska Native, Native Hawaiian or other Pacific, and Hispanic. For descriptive analysis, age was categorized into four groups: those under 50, those between 50 and 64, those between 65 and 79, and those over the age of 80. The available variable for gender included male and female, with no further gender detail available.

Social Determinants of Health Variables

Variables for social determinants of health were retrieved from USVETS. For USVETS variables with a high percentage of missing information, socio-demographic data is purchased from a third party and incorporated into the VA USVETS data infrastructure. The third-party vendors have proprietary algorithms that capture the best available information from public and private entities. In our analysis, we examined education level, the imputed education level, estimated household income, household size, the highest known number of children in the household and marital status (United States Department of Veteran's Affairs Information Resource Center, 2019).

Pre-existing USVETS categorizations were utilized for education level: those who completed high school, those who completed college, those who completed graduate school and those who attended vocational or technical school. The USVETS education variable had a high percentage (22%) of missing data. For those missing data, we were not able to determine if those Veterans had completed less than a high school education or were entirely missing the data. Because of this limitation, we assessed the education variable in combination with the imputed education variable created by the third-party vendor.

The estimated household income was categorized into three groups: less than $39,999, between $40,000 and $74,999 and greater than $75,000. Household size was categorized into four groups: 1 person, 2 people, 3 people, or four or more people. The highest known number of children in the household was categorized into three groups: no children, 1 child or 2 or more children. For those that were missing information for their marital status, the USVETS dataset 'infers' their status using other household information. If there are two people known to live in the household of the opposite sex and within a certain age range of each other, the Veteran is set to ‘inferred married.’ If there is only one name in the household, then the Veteran is set to ‘inferred single.’ For this analysis, we combined inferred married individuals with those with known married status and combined inferred single individuals with those with known single status.

Census and Spatial Variables

At the individual level, we utilized geographic variables in USVETS, including the Rural-urban community area (RUCA) code, 5-digit ZIP code and associated 5 digit Federal Information Processing System (FIPS) code to identify the county and state of residence of each Veteran in our sample. To identify relevant VA facilities for our analysis, we identified the ‘home’ facilities for all Veterans in our study population based on where they receive their primary care. Locations of relevant VA facilities were assessed using a pre-existing spatial file with associated geographic locations (United States Department of Veteran’s Affairs, n.d.).

E. Analysis

All individual-level variables were linked using the PatientICN, a record-identifier created by the VA to identify individual Veterans without protected health information. County-level variables were merged using the county FIPS code which is unique to each county in the U.S. Descriptive analysis was conducted for all Veterans who utilized care during the study period, for Veterans who received COVID-19 testing, and for Veterans who received a positive COVID-19 test. Chi-square analysis assessed whether there was an association between the outcomes and each explanatory variable. All descriptive statistical analysis was conducted using SAS Enterprise Guide version 8.2 (SAS Institute, Cary, NC, US).

Data for all Veterans who received care were aggregated to the county-level. Testing rate was calculated as the total number of Veterans tested divided by the total number of Veterans who accessed care for each county. Test positivity rate was calculated by dividing the total number of Veterans who received a positive test by the total number of Veterans who were tested, again, for each county. Descriptive maps summarizing local testing and positivity rates were produced for the Veteran testing rate and test positivity rate for each county using R version 4.0.5 in R Studio (RStudio Team, 2022).

Lastly, spatial cluster analysis was conducted over space and time using Spatial and Space-Time Scan statistics (SaTScan) (Kulldorff, 1997; Kulldorff & Information Management Services Inc, 2009). This software detects clusters of cases over space and time that are higher than expected using a pre-defined circular scan. Analysis was conducted using a discrete model where the number of COVID-19 cases in each county is Poisson- distributed, using the baseline population of all Veterans who accessed care during the study period at the county-level. The software scans over space and time using a circular "cylinder" where the circular base represents the geographic area of the cluster and the height represents the time interval associated with the cluster. SaTScan identifies clusters over space and time that are least likely to be due to chance, using 999 Monte Carlo simulations. SaTScan analysis was conducted using monthly data at the county-level and the maximum percentage of the population included in clusters was set at 20%. SaTScan version 10.0.02 was utilized (Kulldorff, 1997; Kulldorff & Information Management Services Inc, 2009). Maps of SaTScan results were produced using R version 4.0.5 in R Studio (RStudio Team, 2022). All analysis was conducted within the VA system with several protections in place to protect data confidentiality. Personal identification verification (PIV) cards were distributed to each analyst and data and analysis software were protected behind several software firewalls.

III. Results

In total, 8,059,089 Veterans received care at a VA facility between January 1, 2018, and September 30, 2021 (Figure 1). After removing those with missing values for any explanatory variable, our final analytic dataset included 6,342,455 Veterans. Of these, 1,352,736 (21.33%) received at least one COVID-19 test and of those tested, 275,863 (20.4%) received at least one positive COVID-19 test.

Of the Veterans who received care before or during the COVID-19 pandemic, 91.4% were men, 77.5% were non-Hispanic white, 18.2% were non-Hispanic Black and 1.4% were Hispanic (Table 1). Just over half of those who received care were over the age of 65, and 55.4% were married. The majority (64.7%) of Veterans who received care had no known children.

Of those who received care, 1,352,736 received one or more COVID-19 tests. Of those who were tested, 89.4% were men, 67.4% were non-Hispanic White, 23.2% were non-Hispanic Black and 6.7% were Hispanic (Table 2). Of those who received at least one COVID-19 test, 20.4% had at least one positive COVID-19 test. Of those with at least one positive test, 89.6% were men, 67.2% were non-Hispanic White, 22.5% were non-Hispanic Black and 7.7% were Hispanic (Table 2).

After aggregating to the county-level, there were 3,219 counties that had one or more Veterans receiving care (Figure 2). Of the 3,219 counties, nine counties had no Veterans tested during the study period (designated with black) and 55 counties had no Veterans who tested positive (designated with gray) for COVID-19. A total of 130 VA facilities were identified that had one or more Veterans in the analytic dataset that received primary care (designated with red dots). In Figure 2a, darker purple shades indicate counties with higher testing rates and in Figure 2b, darker green shades indicate counties with higher positivity rates.

Results of SaTScan analyses are represented in Figure 3 and Table 3. The first recorded COVID-19 case was in February of 2020 and the last recorded case was in October of 2021. Three significant clusters were identified when the maximum percentage of the population for each cluster was set to 20% (Figure 3). All identified clusters were identified for the period from November, 2020 to January, 2021. The cluster that was most unlikely to be due to chance was centered in Shelby County, Missouri from November of 2020 to January of 2021,with a relative risk (RR) of 3.45 (Table 3). The second identified cluster was centered in Buckingham County, Virginia (RR: 3.01) and the third identified cluster was centered in Sanpete County, Utah (RR: 3.09).

IV. Discussion

This study analyzed demographic and social determinants of health for approximately 6.3 million Veterans in the United States who accessed care at a VA facility between January 1, 2018, and September 30, 2021. Clusters over space and time were identified in several areas of the country and all identified significant clusters were during a three-month period between November 2020 and January 2021.

Descriptive analysis of the study population indicated similar results with existing literature on SDOH and COVID-19 incidence in the U.S. Veteran population. Black non-Hispanic individuals comprised 18.2% of the study population but 23.2% of those who received a COVID-19 test, while Hispanic individuals were 1.4% of the study population and 6.7% of those who received a COVID-19 test. These findings are consistent with other studies that have identified that Black and Hispanic Veterans were more likely to receive COVID-19 testing over the course of the pandemic (Ferguson et al., 2021; Ioannou et al., 2020; Razjouyan et al., 2021; Rentsch, Kidwai-Khan, et al., 2020). Further, while Hispanic Veterans were 6.7% of those who received testing, they were 7.7% of those who received at least one positive test during the study period, indicating that Hispanic individuals were more likely to test positive than their non-Hispanic counterparts. While other studies reported a similar finding for Black non-Hispanic Veterans (Ferguson et al., 2021; Razjouyan et al., 2021; Rentsch, Kidwai-Khan, et al., 2020), our findings differed and found that while Black non-Hispanic Veterans made up 23.2% of those tested, they made up 22.5% of those who received at least one positive COVID-19 test.

Four interesting findings emerged from the maps of testing and positivity rates in counties. First, there are geographic differences in the distribution of testing and positivity rates in United States counties. Second, qualitatively, our maps demonstrate that high rates of testing for COVID-19 do not always correlate with high rates of positivity in administered COVID-19 tests in the Veteran population. For example, it appears that in states such as California and Florida, many counties have relatively high testing rates but relatively low positivity rates. Conversely, in states such as Michigan and Georgia, many counties have relatively low testing rates but relatively high positivity rates. Third, there is a clear concentration of counties with high rates of test positivity throughout the middle of the country. Lastly, it appears clusters of counties with high testing rates were highly clustered around facilities while clusters of counties with high positivity rates were not. We hypothesize that clustering of testing around VA facilities could, in part, be because Veterans who live closer to VA facilities are more likely to obtain testing at VA facilities, instead of utilizing testing elsewhere.

Spatial cluster analysis over space and time indicated that all identified statistically significant clusters of Veterans most at risk of testing positive for COVID-19 covered a three-month time period from November 2020 to January 2021. This suggests that the peak of cases in the larger U.S. population that occurred in the winter of 2020 extended to the Veteran population

(Centers for Disease Control and Prevention, n.d.). Further, Veterans were most at risk of receiving a positive COVID-19 test in the identified U.S. regions during this period (Figure 3). When using a radius of 20% of the study population, spatial cluster analysis indicated that Veterans with home facilities in the Midwest region who received a test between November 1, 2020 and January 31, 2021 were more than three times more at risk of testing positive than those Veterans with home facilities outside of the Midwest region who received a test in the same time period. The most likely cluster was in the middle of the country (centered in Shelby County, Missouri), largely mirroring the regional high rates of positivity in the county-level positivity rate map (Figure 2b).

To our knowledge, no other studies have conducted spatial cluster analysis for the U.S. Veteran population. However, there is literature on spatial cluster analysis of the U.S. general population. One study used spatial clustering methods (specifically, local Moran statistics) to identify significant clusters of COVID-19 cases, but this did not assess clustering over time and instead opted to identify spatial clusters during four separate and predetermined time periods. However, for the period between September 10, 2020 and January 4, 2021 which is most aligned with identified primary clusters in our analysis, similar clustering of cases in the mid-west and middle of the country were identified (Andrews et al., 2021).

Our analysis has at least three strengths. First, in using data from the VA, we were able to access a large administrative, consistently collected, and reliable dataset for Veterans in the entire United States. As a result, our study results are generalizable to Veterans who access care in the U.S. Second, our results have the potential to be translated back to specific, local VA facilities and offices in the U.S. and therefore have potential for real-world policy change.

Finally, this analysis utilized space-time scan statistics and was therefore able to detect clustering over space and time, instead of only over space without a temporal component.

Several limitations arose over the course of our analysis. First, Veterans who received care may not have received testing from VA facilities and instead, have gone to other facilities to receive testing. Access to testing outside of the VA may vary by geographic location or by urban/ rural divides, and Veterans may defer to VA services if they are unable to access testing elsewhere. As a result, our results are subject to differential selection bias and descriptive findings may not be an accurate representation of the true number of cases in the U.S. Veteran population. Second, we were limited to the use of imputed variables for income and education and were not able to utilize many SDOH variables in the USVETS dataset because of high percentages of missing data. Third, individuals' index dates reflected the date of their first positive test only and did not account for subsequent testing. Veterans could have received additional positive or negative tests after the index date but the existing data structure did not allow for analysis of this data. Fourth, VA facilities for each Veteran are recorded by the VA as their "home" site. However, Veterans could have received testing at any VA facility in the country to be included in this dataset, and no testing site variable was available at the time of analysis. Fifth, for Veterans with unknown marital status, an 'inference' is made to assume that if two individuals of opposite genders and within a specific age range of each other are living in the same household, they are 'married.' This decision does not account for same-sex marriages or long-term partnerships. Lastly, because Veterans are primarily male and white, these results are not as generalizable to the U.S. population.

These findings elucidate numerous additional research questions and next steps. First, this analysis should be extended to include up-to-date data accounting for well-documented increases in COVID-19 cases due to the Delta and Omicron variants of COVID-19 across the United States (Centers for Disease Control and Prevention, n.d.). Second, statistical analysis should be conducted to assess whether clusters of testing and test positivity were associated with proximity to VA facilities (Waller & Gotway, 2004). In addition, a clear next step in this research is to assess the role of individual-level social determinants of health in the proliferation and prominence of identified space-time clusters. Research questions could expand in many directions. Of note, one study conducted a retrospective spatial cluster analysis of COVID-19 cases by ZIP code in the four counties surrounding Kansas City, Missouri with respect to demographic factors (Alqadi, Bani-Yaghoub, Balakumar, Wu, & Francisco, 2021). This study identified several clusters of cases at the ZIP code level for specific gender and racial groups and found that Hispanic populations had the most scattered clusters and the highest prevalence of COVID-19, compared to Black and white populations in Kansas City. Therefore, additional analyses with our dataset could examine Veteran subpopulations at the county-level.

Further, regression analysis techniques could be employed to assess how social determinants of health predispose Veterans to test positive for COVID-19 differently, based on whether or not they are living in a place with an outbreak or cluster of cases. To better understand how social determinants of health place Veterans at increased risk of COVID-19 test positivity, regression analysis techniques could also be used to adjust for clustering and environmental factors. Multi-level regression analysis and geographic-weighted regression are other sets of techniques to address questions looking at the relationships between individual and county-level social determinants of health data concurrently (Fotheringham, Brunsdon, & Charlton, 2002; Gelman & Hill, 2006). Further, this SaTScan methodology could be applied at smaller geographic scales to describe Veteran risk at the neighborhood level. As noted, a limitation of this analysis was that Veterans could have received COVID-19 testing at facilities other than their “home” Veterans Administration healthcare center. To address this issue, additional analyses could examine Veteran healthcare utilization among those who have a history of high utilization of VA services. Alternatively, healthcare utilization could be adjusted for or assessed as an effect modifier in regression analyses.

Findings from this analysis have important policy implications and relevance to public health. VA leadership and local policy-makers can use these results to institute additional surveillance and resources for communities at increased risk of testing positive. If resources are limited, this analysis can be used to allocate resources to communities most at risk. Moving forward, this analysis provides a backdrop for future studies to better understand the ongoing pandemic and to identify areas in the United States where Veterans are most at risk of testing positive in a given period.

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VI. Tables and Figures

Table 1: *Study characteristics of Veterans who received care between January 1, 2018 and September 30, 2021, stratified by receipt of one or more COVID-19 tests*

Variable	General VA Pop N = 6,342,455		Those who received ≥ 1 COVID-19 test N = 1,352,736 (21.33%)		Those who did not receive a COVID-19 test N = 4,989,719 (78.67%)		Chi-Square
	N	%	N	%	N	%	p-value
Gender							p < .001
Male	5,797,442	91.4%	1,209,504	89.4%	4,587,938	92.0%	
Female	545,013	8.6%	143,232	10.6%	401,781	8.1%	
Race/ Ethnicity							p < .001
Non-Hispanic White	4,912,632	77.5%	912,076	67.4%	4,000,556	80.2%	
Non-Hispanic Black or African American	1,150,931	18.2%	313,749	23.2%	837,182	16.8%	
Asian	80,753	1.3%	15,156	1.1%	65,597	1.3%	
American-Indian or Alaska Native	52,539	0.8%	9,845	0.7%	42,694	0.9%	
Native Hawaiian or Other Pacific	54,369	0.9%	10,679	0.8%	43,690	0.9%	
Hispanic	91,231	1.4%	91,231	6.7%	0	0%	
Age							p < .001
< 50	1,501,162	23.7%	311,702	23.0%	1,189,460	23.8%	
50 – 64	1,515,830	23.9%	398,609	29.5%	1,117,221	22.4%	
65 – 79	2,449,419	38.6%	538,814	39.8%	1,910,605	38.3%	
> 80	876,044	13.8%	103,611	7.7%	772,433	15.5%	
Marital Status							p < .001
Married (or Inferred Married)	3,512,585	55.4%	666,464	49.3%	2,846,120	57.0%	
Single (or Inferred Single)	2,829.870	44.6%	686,271	50.7%	2,143,599	43.0%	
Education (Imputed)							p < .001
Completed High School	4,460,572	70.3%	977,507	72.3%	3,483,065	69.8%	
Completed College	1,106,680	17.5%	218,280	16.1%	888,400	17.8%	
Completed Graduate School	754,355	11.9%	152,577	11.3%	601,778	12.1%	
Attended Vocational/ Technical School	20,848	0.3%	4,372	0.3%	16,476	0.3%	
Education							p < .001
Completed High School	2,642,498	41.7%	549,451	40.6%	2,093,047	42.0%	
Completed College	1,624,198	25.6%	336,027	28.8%	1,288,171	25.8%	
Completed Graduate School	608,748	9.6%	114,844	8.5%	493,904	9.9%	

Attended Vocational/ Technical School	51,021	0.8%	11,713	0.9%	39,308	0.8%	
Missing	1,415,990	22.3%	340,701	25.2%	1,075,289	21.6%	
Household Size							p < .001
1 person	1,580,071	24.9%	391,818	29.0%	1,188,253	23.8%	
2 people	1,826,484	28.8%	366,673	27.1%	1,459,811	29.3%	
3 people	1,409,045	22.2%	281,637	20.8%	1,127,408	22.6%	
4 or more people	1,526,855	24.1%	312,608	23.1%	1,214,247	24.3%	
Number of Children in Household (Highest Known)							p < .001
No children	4,105,117	64.7%	868,649	64.2%	3,236,468	64.9%	
1 child	1,741,165	27.5%	375,323	27.8%	1,365,842	27.4%	
2 or more children	496,173	7.8%	108,764	8.0%	387,409	7.8%	
Income (Estimated Household Income)							p < .001
Less than $39,999	2,166,749	34.2%	485,002	35.9%	1,681,747	33.7%	
$40,000 to $74,999	2,450,197	38.6%	528,418	39.1%	1,921,779	38.5%	
Greater than $75,000	1,725,509	27.2%	339,316	25.1%	1,386,193	27.8%	
RUCA							p < .001
Rural	1,221,215	19.3%	217,004	16.0%	1,004,211	20.1%	
Urban	5,121,240	80.8%	1,135,732	84.0%	3,985,508	79.9%	

Table 2: *Study characteristics of Veterans who received a COVID-19 test between January 1, 2018 and September 30, 2021, stratified by receipt of one or more positive COVID-19 tests*

Variable	Those who received ≥1 COVID-19 test N = 1,352,736		Received ≥1 Positive COVID-19 test result N = 275,863 (20.4%)		Received ≥1 Negative COVID-19 test result N = 1,076,873 (79.6%)		Chi Square
	N	%	N	%	N	%	
Gender							$p < .001$
Male	1,209,504	89.4%	247,240	89.6%	962,264	89.4%	
Female	143,232	10.6%	28,623	10.4%	114,609	10.6%	
Race/ Ethnicity							$p < .001$
Non-Hispanic White	912,076	67.4%	185,501	67.2%	726,575	67.5%	
Non-Hispanic Black or African American	313,749	23.2%	62,086	22.5%	251,663	23.4%	
Asian	15,156	1.1%	2,598	0.9%	12,558	1.2%	
American-Indian or Alaska Native	9,845	0.7%	2,269	0.8%	7,576	0.7%	
Native Hawaiian or Other Pacific	10,679	0.8%	2,213	0.8%	8,466	0.8%	
Hispanic	91,231	6.7%	21,196	7.7%	70,035	6.5%	
Age							$p < .001$
< 50	311,702	23.0%	74,949	27.2%	236,753	22.0%	
50 – 64	398,609	29.5%	78,942	28.6%	319,667	29.7%	
65 – 79	538,814	39.8%	98,552	35.7%	440,262	40.9%	
> 80	103,611	7.7%	23,420	8.5%	80,191	7.4%	
Marital Status							$p < .001$
Married (or Inferred Married)	666,464	49.3%	143,355	52.0%	523,110	48.6%	
Single (or Inferred Single)	686,271	50.7%	132,508	48.0%	553,763	51.4%	
Education (Imputed)							$p < .001$
Completed High School	977,507	72.3%	203,684	73.8%	773,823	71.9%	
Completed College	218,280	16.1%	43,484	15.8%	174,796	16.2%	
Completed Graduate School	152,577	11.3%	27,801	10.1%	124,776	11.6%	
Attended Vocational/ Technical School	4,372	0.3%	894	0.3%	3,478	0.3%	
Education							$p < .001$
Completed High School	549,451	40.6%	117,204	42.5%	432,247	40.1%	
Completed College	336,027	28.8%	69,067	25.0%	266,960	24.8%	
Completed Graduate School	114,844	8.5%	22,144	8.0%	92,700	8.6%	
Attended Vocational/ Technical School	11,713	0.9%	2,453	0.9%	9,260	0.9%	
Missing	340,701	25.2%	64,995	23.6%	275,706	25.6%	

Household Size							
1 person	391,818	29.0%	72,562	26.3%	319,256	29.7%	
2 people	366,673	27.1%	73,404	26.6%	293,269	27.2%	
3 people	281,637	20.8%	59,431	21.5%	222,206	20.6%	
4 or more people	312,608	23.1%	70,466	25.5%	242,142	22.5%	
Number of Children in Household (Highest Known)							p < .001
No children	868,649	64.2%	169,822	61.6%	698,827	64.9%	
1 child	375,323	27.8%	80,320	29.1%	295,003	27.4%	
2 or more children	108,764	8.0%	25,721	9.3%	83,043	7.7%	
Income (Estimated Household Income)							p < .001
Less than $39,999	485,002	35.9%	99,625	36.1%	385,377	35.8%	
$40,000 to $74,999	528,418	39.1%	108,667	39.4%	419,751	39.0%	
Greater than $75,000	339,316	25.1%	67,571	24.5%	271,745	25.2%	
RUCA							p < .001
Rural	217,004	16.0%	49,869	18.1%	167,135	15.5%	
Urban	1,135,732	84.0%	225,994	81.9%	909,738	84.5%	

Table 3: *Hotspot clusters of COVID-19 cases - center county, time period and relative risks, maximum of 20% of population*

Cluster	Center County	Time	Relative Risk	P-value
1: Most likely cluster	Shelby County, Missouri	November 2020 – January 2021	3.45	p < 0.001
2: Secondary cluster	Buckingham County, Virginia	November 2020 – January 2021	3.01	p < 0.001
3: Least likely cluster	Sanpete County, Utah	November 2020 – January 2021	3.09	p < 0.001

Figure 1: Consort diagram of study population and selection of study participants

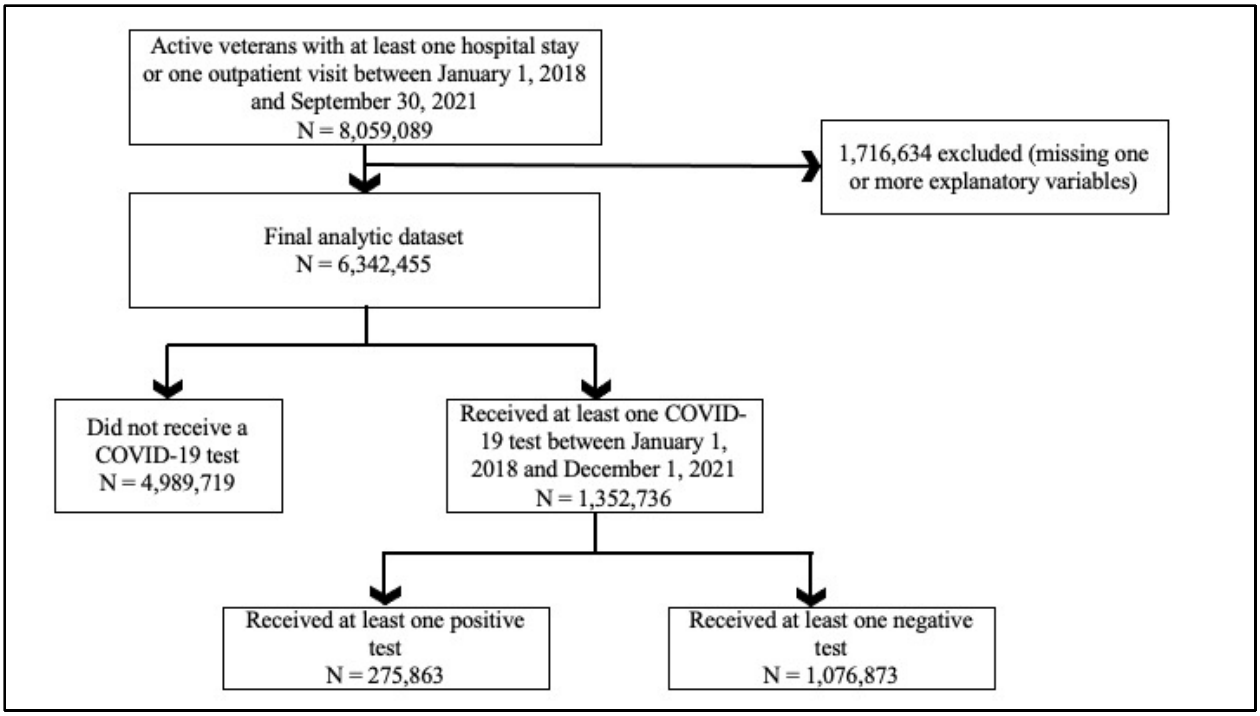
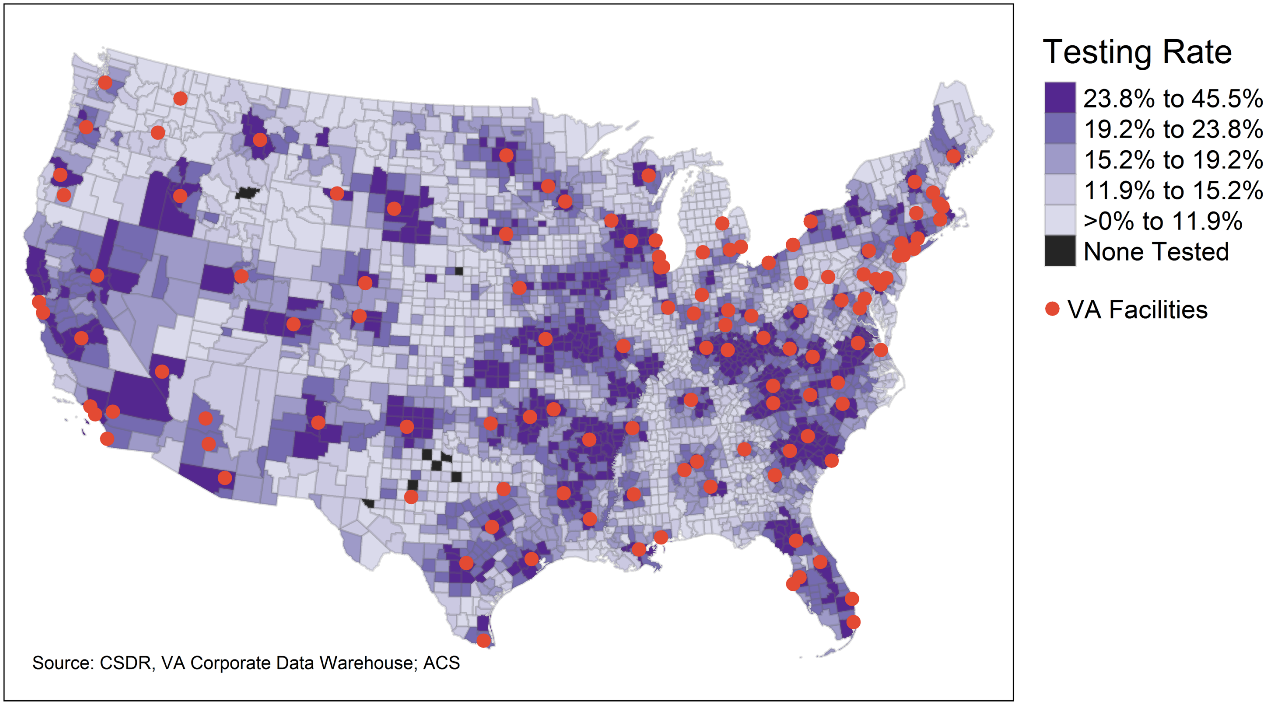


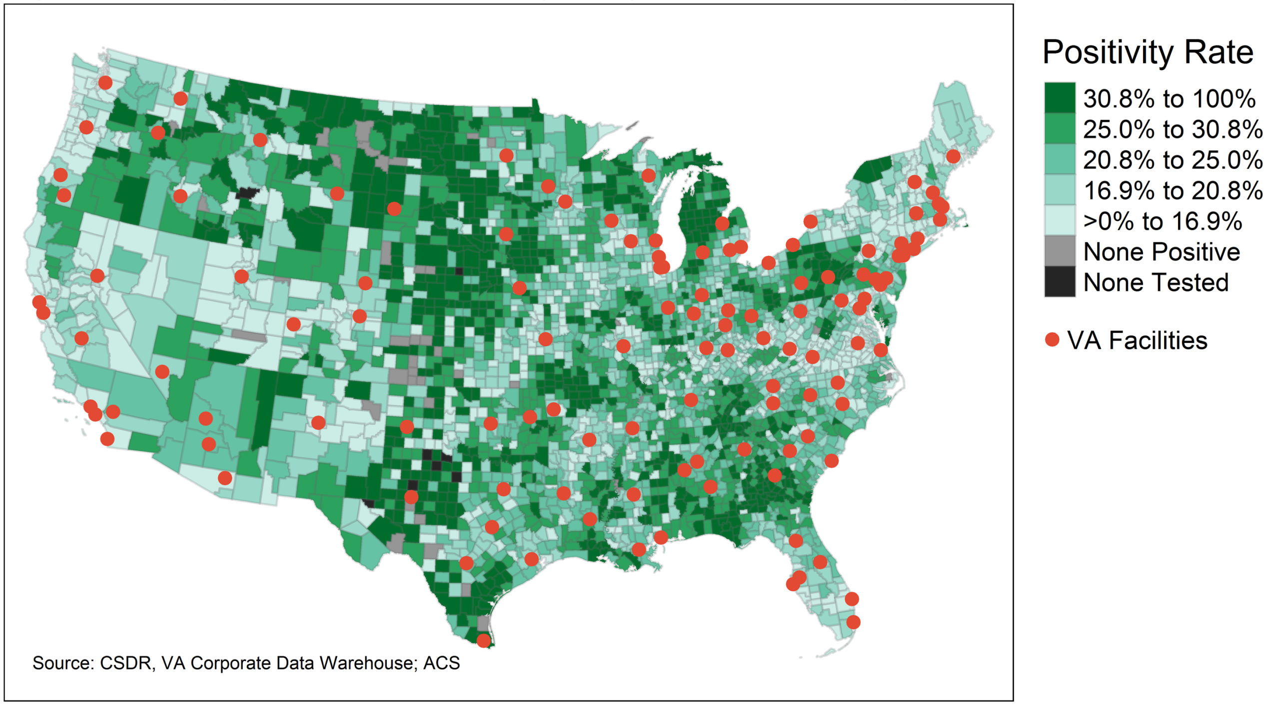
Figure 2: *Maps of testing and positivity rates by county, United States*

Figure 2a: Testing Rate of Veterans by County, United States, January 2, 2018 - December 1, 2021



Source: CSDR, VA Corporate Data Warehouse; ACS

Figure 2b: Positivity Rate of Tested Veterans by County, United States, January 2, 2018 - December 1, 2021



Source: CSDR, VA Corporate Data Warehouse; ACS

Figure 3: *Identified county hotspot clusters of COVID-19 cases in United States Veterans, maximum of 20% of population (February 2020 – October 2021)*